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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 23:34:14 ; Search time 127 Seconds

(without alignments)  
257.681 Million cell updates/sec

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	20	100.0	2518	US-09-433-699-3	Sequence 3, Appl
4	20	100.0	2527	US-09-949-016-4169	Sequence 4169, Ap
5	20	100.0	13489	US-09-949-016-15911	Sequence 15911, A
6	18	90.0	20	US-09-433-699-14	Sequence 14, Appl
7	15	75.0	597	US-09-134-000C-2181	Sequence 2181, Ap
8	15	75.0	1176	US-09-489-039A-2620	Sequence 2620, Ap
9	15	75.0	1211	US-09-270-767-31566	Sequence 31566, A
10	15	75.0	1395	US-09-489-039A-2450	Sequence 2450, Ap
11	15	75.0	1498	US-09-270-767-15231	Sequence 15231, A
12	15	75.0	2118	US-09-902-540-3960	Sequence 3960, Ap
13	15	75.0	18324	US-09-902-540-1196	Sequence 1196, Ap
14	15	75.0	160018	US-09-949-016-12617	Sequence 12617, A
15	15	75.0	160018	US-09-949-016-15994	Sequence 15994, A
16	14	70.0	392	US-09-702-705-1570	Sequence 1570, Ap
17	14	70.0	392	US-09-736-457-1570	Sequence 1570, Ap
18	14	70.0	392	US-09-614-124B-1570	Sequence 1570, Ap
19	14	70.0	392	US-09-671-325-1570	Sequence 1570, Ap
20	14	70.0	392	US-09-658-824-1570	Sequence 1570, Ap
21	14	70.0	819	US-08-998-416-336	Sequence 336, App
22	14	70.0	1057	US-09-452-239-5	Sequence 5, Appl
23	14	70.0	1229	US-08-790-572-2	Sequence 5, Appl
24	14	70.0	1229	US-09-213-396-2	Sequence 2, Appl
25	14	70.0	1230	US-09-016-434-585	Sequence 585, App
26	14	70.0	1336	US-09-180-109A-28	Sequence 28, Appl
27	14	70.0	1420	US-09-180-109A-23	Sequence 23, Appl

C	28	14	70.0	1452	4	US-09-252-991A-4444	Sequence 4444, Ap
C	29	14	70.0	1671	4	US-09-252-991A-4648	Sequence 4648, Ap
C	30	14	70.0	1680	4	US-09-902-540-8972	Sequence 8972, Ap
C	31	14	70.0	2115	4	US-09-252-991A-4163	Sequence 4163, Ap
C	32	14	70.0	2166	4	US-09-902-540-8129	Sequence 8129, Ap
C	33	14	70.0	2343	4	US-09-976-594-986	Sequence 986, App
C	34	14	70.0	2529	4	US-09-815-923-15	Sequence 15, Appl
C	35	14	70.0	2690	4	US-08-524-757-11	Sequence 11, Appl
C	36	14	70.0	2885	1	US-09-016-434-1143	Sequence 1143, Ap
C	37	14	70.0	3501	1	US-08-524-757-5	Sequence 5, Appl
C	38	14	70.0	3802	1	US-08-404-354B-2	Sequence 2, Appl
C	39	14	70.0	3802	1	US-08-314-083B-2	Sequence 2, Appl
C	40	14	70.0	3802	1	US-08-435-675B-2	Sequence 2, Appl
C	41	14	70.0	3802	1	US-08-336-257A-4	Sequence 4, Appl
C	42	14	70.0	3802	3	US-08-884-599-2	Sequence 2, Appl
C	43	14	70.0	3802	6	5386025-7	Sequence 2, Appl
C	44	14	70.0	3802	6	5386025-7	Sequence 2, Appl
C	45	14	70.0	5499	4	US-09-902-540-2892	Sequence 2892, Ap

#### ALIGNMENTS

RESULT 1  
US-09-621-976-13204/C  
Sequence 13204, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Malne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTE and Encoded Human Proteins.  
FILE REFERENCE: GENSET 054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 13204  
LENGTH: 442  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-621-976-13204

Query Match 100.0%; Score 20; DB 4; Length 442;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGGTGTA 20  
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Db 166 ATGATGGCGGCGAGGTGTA 147

RESULT 2  
US-09-513-999C-1128/C  
Sequence 1128, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Malne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1998-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 1128  
LENGTH: 467  
TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: 162..467  
US-09-513-999C-1128

Query Match 100.0%; Score 20; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
|||||  
DB 163 ATGATGGCGCGGAGTGTGA 144

RESULT 3  
US-09-433-699-3/c  
Sequence 3, Application US/09433699B  
Patent No. 6165786  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Lex M. Cowser  
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION  
FILE REFERENCE: RTS-0109  
CURRENT APPLICATION NUMBER: US/09/433,699B  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 3  
LENGTH: 2518  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (112)..(2235)  
US-09-433-699-3

Query Match 100.0%; Score 20; DB 3; Length 2518;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
|||||  
DB 113 ATGATGGCGCGGAGTGTGA 94

RESULT 4  
US-09-949-016-4169/c  
Sequence 4169, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4169  
LENGTH: 2527  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4169

Query Match 100.0%; Score 20; DB 4; Length 2527;  
Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
|||||  
DB 113 ATGATGGCGCGGAGTGTGA 94

RESULT 5  
US-09-949-016-15911/c  
Sequence 15911, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15911  
LENGTH: 13489  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15911

Query Match 100.0%; Score 20; DB 4; Length 13489;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
|||||  
DB 2113 ATGATGGCGCGGAGTGTGA 2094

RESULT 6  
US-09-433-699-14  
Sequence 14, Application US/09433699B  
Patent No. 6165786  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Lex M. Cowser  
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION  
FILE REFERENCE: RTS-0109  
CURRENT APPLICATION NUMBER: US/09/433,699B  
CURRENT FILING DATE: 1999-11-03  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 14  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-433-699-14

Query Match 90.0%; Score 18; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGT 18  
|||||  
DB 3 ATGATGGCGCGGAGTGT 20

RESULT 7  
US-09-134-000C-2181  
Sequence 2181, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2181  
LENGTH: 597  
TYPE: DNA  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-2181

Query Match 75.0%; Score 15; DB 4; Length 597;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGCGCGCGAGTG 17  
|||||  
DB 496 GATGCGCGCGAGTG 510

RESULT 8  
US-09-489-039A-2620/C  
Sequence 2620, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 2620  
LENGTH: 1176  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2620

Query Match 75.0%; Score 15; DB 4; Length 1176;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAG 15  
|||||  
DB 95 ATGATGCGCGCGAG 81

RESULT 9  
US-09-270-767-31566/C  
Sequence 31566, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31566  
LENGTH: 1211  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-31566

Query Match 75.0%; Score 15; DB 4; Length 1211;

Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGCGCGCGAGTG 17  
|||||  
DB 72 GATGCGCGCGAGTG 58

RESULT 10  
US-09-489-039A-2450/C  
Sequence 2450, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 2450  
LENGTH: 1395  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2450

Query Match 75.0%; Score 15; DB 4; Length 1395;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAG 15  
|||||  
DB 1325 ATGATGCGCGCGAG 1311

RESULT 11  
US-09-270-767-15231/C  
Sequence 15231, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 15231  
LENGTH: 1498  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-15231

Query Match 75.0%; Score 15; DB 4; Length 1498;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGCGCGCGAGTG 17  
|||||  
DB 72 GATGCGCGCGAGTG 58

RESULT 12  
US-09-902-540-3960  
Sequence 3960, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.

```

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3960
; LENGTH: 2118
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3960

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 2118;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGGCGCGGAGTGTG 17
DB 516 GATGGCGCGGAGTGTG 530

RESULT 13
US-09-902-540-1196
; Sequence 1196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1196
; LENGTH: 18324
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1196

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 18324;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GATGGCGCGGAGTGTG 17
DB 3168 GATGGCGCGGAGTGTG 3182

RESULT 14
US-09-949-016-12617/c
; Sequence 12617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12617

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; LENGTH: 160018
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(160018)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12617

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 160018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCGGAGTGTGA 20
DB 1171 GGCGGCGGAGTGTGA 1157

RESULT 15
US-09-949-016-15994/c
; Sequence 15994, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15994
; LENGTH: 160018
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(160018)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15994

Query Match
Best Local Similarity 100.0%; Score 15; DB 4; Length 160018;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCGGAGTGTGA 20
DB 1171 GGCGGCGGAGTGTGA 1157

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2005, 23:49:38 ; Search time 508 Seconds  
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Title: US-10-797-822-1

Perfect score: 20

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-10-797-822-1	Sequence 1, Appli
2	20	100.0	20	US-10-797-822-2	Sequence 2, Appli
3	20	100.0	240	US-10-357-930-35092	Sequence 35092, A
4	20	100.0	377	US-09-918-995-37497	Sequence 37497, A
5	20	100.0	396	US-10-357-930-4788	Sequence 4788, Ap
6	20	100.0	438	US-10-357-930-4939	Sequence 4939, A
7	20	100.0	444	US-10-357-930-1957	Sequence 1957, A
8	20	100.0	636	US-10-198-846-9321	Sequence 9321, Ap
9	20	100.0	1276	US-10-363-345A-27853	Sequence 27853, A
10	20	100.0	1276	US-10-363-345A-27854	Sequence 27854, A
11	20	100.0	1276	US-10-363-483A-27853	Sequence 27853, A

C 12	20	100.0	1276	19	US-10-363-483A-27854	Sequence 27854, A
C 13	20	100.0	1860	18	US-10-357-930-28900	Sequence 28900, A
C 14	20	100.0	2518	9	US-09-825-866-28	Sequence 28, Appl
C 15	20	100.0	2518	18	US-10-400-083-18	Sequence 18, Appl
C 16	20	100.0	2637	17	US-10-104-047-681	Sequence 681, App
C 17	20	100.0	2723	17	US-10-384-569-5	Sequence 5, Appl1
C 18	20	100.0	3201	18	US-10-357-930-22147	Sequence 22147, A
C 19	20	100.0	3201	18	US-10-357-930-23035	Sequence 23035, A
C 20	20	100.0	3497	14	US-10-198-846-13141	Sequence 13141, A
C 21	20	100.0	6112	15	US-10-172-086-34	Sequence 34, Appl
C 22	20	100.0	6112	18	US-10-311-507-66	Sequence 66, Appl
C 23	20	100.0	6112	18	US-10-480-846-34	Sequence 34, Appl
C 24	20	100.0	10942	9	US-09-825-866-23	Sequence 23, Appl
C 25	20	100.0	10942	17	US-10-384-569-4	Sequence 85334, A
C 26	18	90.0	1212	18	US-10-437-963-85334	Sequence 1202, Ap
C 27	16	80.0	378	18	US-10-437-963-1202	Sequence 1202, Ap
C 28	16	80.0	422	17	US-10-424-599-2016	Sequence 2016, A
C 29	15	75.0	198	18	US-10-437-963-942	Sequence 942, App
C 30	15	75.0	279	18	US-10-437-963-19210	Sequence 39210, A
C 31	15	75.0	468	18	US-10-437-963-19917	Sequence 39917, A
C 32	15	75.0	516	15	US-10-156-761-2381	Sequence 2381, Ap
C 33	15	75.0	622	17	US-10-425-114-16873	Sequence 16873, A
C 34	15	75.0	657	18	US-10-437-963-11826	Sequence 11826, A
C 35	15	75.0	688	17	US-10-425-114-24523	Sequence 24523, A
C 36	15	75.0	693	17	US-10-425-114-25348	Sequence 25348, A
C 37	15	75.0	693	18	US-10-425-115-29080	Sequence 29080, A
C 38	15	75.0	702	18	US-10-425-115-113470	Sequence 113470, A
C 39	15	75.0	725	18	US-10-363-345A-14091	Sequence 14091, A
C 40	15	75.0	725	18	US-10-363-345A-14092	Sequence 14092, A
C 41	15	75.0	725	19	US-10-363-483A-14091	Sequence 14091, A
C 42	15	75.0	725	19	US-10-363-483A-14092	Sequence 14092, A
C 43	15	75.0	726	18	US-10-363-483A-20161	Sequence 20161, A
C 44	15	75.0	726	18	US-10-363-483A-20162	Sequence 20162, A
C 45	15	75.0	726	19	US-10-363-483A-20161	Sequence 20161, A

#### ALIGNMENTS

RESULT 1  
US-10-797-822-1  
; Sequence 1, Application US/10797822  
; Publication No. US20050026860A1  
; GENERAL INFORMATION:  
; APPLICANT: Chin-Tang Lin  
; APPLICANT: Han-Chung Wu  
; TITLE OF INVENTION: Nucleolin Antisense Sequence FOR Inhibition of CANCER Cell Prolif  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/797,822  
; CURRENT FILING DATE: 2004-03-09  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense fragment which sequence is specifically complementary t  
US-10-797-822-1

Query Match 100.0%; Score 20; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGCTGTA 20  
|||||  
DB 1 ATGATGGCGGCGAGCTGTA 20

RESULT 2  
US-10-797-822-2/c  
; Sequence 2, Application US/10797822  
; Publication No. US20050026860A1

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; GENERAL INFORMATION:
; APPLICANT: Chin-Tating Lin
; TITLE OF INVENTION: Nucleolin Antisense Sequence FOR Inhibition of CANCER Cell Prolif
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/797,822
; CURRENT FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sense fragment which sequence is similar to the nucleolin mRNA
US-10-797-822-2

Query Match          100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGCGAGTGTGA 20
    |||||||||||||||
Db 20 ATGATGGCGCGCGAGTGTGA 1

RESULT 3
US-10-357-930-35092/C
; Sequence 35092, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endegge, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35092
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-35092

Query Match          100.0%; Score 20; DB 18; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGCGAGTGTGA 20
    |||||||||||||||
Db 116 ATGATGGCGCGCGAGTGTGA 97

RESULT 4
US-09-918-995-37497/C
; Sequence 37497, Application US/09918995
```

```

; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37497
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-37497

Query Match          100.0%; Score 20; DB 10; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGCGAGTGTGA 20
    |||||||||||||||
Db 98 ATGATGGCGCGCGAGTGTGA 79

RESULT 5
US-10-357-930-4788/C
; Sequence 4788, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endegge, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4788
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 224_242, 273, 286, 312, 321
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-4788

Query Match          100.0%; Score 20; DB 18; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGCGAGTGTGA 20
    |||||||||||||||
```

Db 86 ATGATGCGCGGAGTGTA 67

RESULT 6

US-10-357-930-43939/c

Sequence 43939, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255,281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 43939

LENGTH: 438

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-43939

Query Match 100.0%; Score 20; DB 18; Length 438;

Best Local Similarity 100.0%; Pred. No. 0.073;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGGAGTGTA 20

|||||

Db 80 ATGATGCGCGGAGTGTA 61

RESULT 7

US-10-357-930-13957/c

Sequence 13957, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219,007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255,281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13957

LENGTH: 444

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-13957

Query Match 100.0%; Score 20; DB 18; Length 444;

Best Local Similarity 100.0%; Pred. No. 0.072;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGGAGTGTA 20

|||||

Db 70 ATGATGCGCGGAGTGTA 51

RESULT 8

US-10-198-846-9321/c

Sequence 9321, Application US/10198846

Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MRI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9321

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc\_feature

LOCATION: 3, 9, 56, 59

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-9321

Query Match 100.0%; Score 20; DB 14; Length 636;

Best Local Similarity 100.0%; Pred. No. 0.068;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGGAGTGTA 20

|||||

Db 133 ATGATGCGCGGAGTGTA 114

RESULT 9

US-10-363-345A-27853

Sequence 27853, Application US/10363345A

Publication No. US20040234960A1

GENERAL INFORMATION:

APPLICANT: Alexander Olek

APPLICANT: Christian Piepenbrock

APPLICANT: Kurt Berlin

TITLE OF INVENTION: Method for determining the degree of methylation of defined

TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3

FILE REFERENCE: E01/1227

CURRENT APPLICATION NUMBER: US/10/363,345A

CURRENT FILING DATE: 2003-03-03

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 27853

Query Match	100.0%;	Score 20;	DB 19;	Length 1276;
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RESULT 13
US-10-357-930-28900/c
; Sequence 28900. Application Us/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28900
LENGTH: 1860
TYPE: DNA

```



```
/ ORGANISM: Homo sapiens
US-10-357-930-26900

Query Match          100.0%; Score 20; DB 18; Length 1860;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAGTGTGA 20
        |||
        113 ATGATGCGCGCGAGTGTGA 114

RESULT 14
US-09-825-886-28/c
/ Sequence 28, Application US/09825886
/ Publication No. US20020076693A1
/ GENERAL INFORMATION:
/ APPLICANT: Hovanesian, Ara
/ APPLICANT: Callebaut, Christian
/ APPLICANT: Krust, Bernard
/ APPLICANT: Jacotot, Etienne
/ APPLICANT: Muller, Sylviane
/ APPLICANT: Briand, Jean-Paul
/ APPLICANT: Guichard, Gilles
/ TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES.
/ FILE REFERENCE: 03495.0166-01000
/ CURRENT APPLICATION NUMBER: US/09/825,886
/ PRIOR FILING DATE: 2001-07-26
/ PRIOR APPLICATION NUMBER: 09/393,302
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/EP98/01409
/ PRIOR FILING DATE: 1998-03-12
/ PRIOR APPLICATION NUMBER: 60/040,969
/ PRIOR FILING DATE: 1997-03-12
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 28
/ LENGTH: 2518
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-825-886-28

Query Match          100.0%; Score 20; DB 9; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAGTGTGA 20
        |||
        113 ATGATGCGCGCGAGTGTGA 94

RESULT 15
US-10-400-083-18/c
/ Sequence 18, Application US/10400083
/ Publication No. US20040186056A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruoslahti, Erkki
/ APPLICANT: Porkka, Kimmo
/ APPLICANT: Christian, Sven
/ TITLE OF INVENTION: HMGN2 Peptides and Related Molecules
/ TITLE OF INVENTION: that Selectively Home to Tumor Blood Vessels and Tumor Cells
/ FILE REFERENCE: P-LJ 5662
/ CURRENT APPLICATION NUMBER: US/10/400,083
/ PRIOR FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: US 10/116,866
/ PRIOR FILING DATE: 2002-04-05
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 2518
/ TYPE: DNA
/ ORGANISM: Homo sapiens
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/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (112)...(2235)
US-10-400-083-18

Query Match          100.0%; Score 20; DB 18; Length 2518;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGATGCGCGCGAGTGTGA 20
        |||
        113 ATGATGCGCGCGAGTGTGA 94

Db      113 ATGATGCGCGCGAGTGTGA 94

Search completed: April 12, 2005, 01:29:20
Job time : 510 secs
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Query Match 100.0%; Score 20; DB 4; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
 |||||  
 70 ATGATGGCGCGGAGTGTGA 89

RESULT 2  
 CBI27338 142 bp mRNA linear EST 29-JAN-2003  
 LOCUS K-EST0176605 C1SNUI7 Homo sapiens cDNA clone C1SNUI7-9-G05 5', mRNA  
 DEFINITION sequence.  
 ACCESSION CBI27338  
 VERSION CBI27338.1 GI:28089748  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 142)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.Y., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 9 row: G column: 05  
 High quality sequence stop: 142.  
 Location/Qualifiers  
 1..142  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="C1SNUI7-9-G05"  
 /sex="F"  
 /tissue\_type="uterine"  
 /cell\_type="Epithelial"  
 /cell\_line="SNU-17"  
 /lab\_host="Top10F"  
 /clone\_id="C1SNUI7"  
 /note="Organ: Cervix; Vector: PCNS-D2; Site 1: EcoRI;  
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then deapped  
 with tadacco acid pyrophosphatase (TAP). The deapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 DNA ligase and the first  
 strand cDNA was synthesized from oligo dt-selected mRNA by  
 priming with dt-tailed vector. The dt-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
 |||||  
 130 ATGATGGCGCGGAGTGTGA 111

RESULT 3  
 AL121075/c 155 bp mRNA linear EST 04-SEP-2003  
 LOCUS DKFZP762B035.r1.762 (synonym: hme12) Homo sapiens cDNA clone  
 DEFINITION DKFZP762B035-5', mRNA sequence.  
 ACCESSION AL121075  
 VERSION AL121075.1 GI:5927076  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 155)  
 AUTHORS Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and  
 Wiemann,S.  
 TITLE EST (Bloecker, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: MIPS  
 MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 5' sequence of the clone insert  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 Braunschweig/Germany) within the cDNA sequencing consortium of the  
 German Genome Project.  
 No si sequence available.  
 This clone (DKFZP762B035) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcencentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
 Location/Qualifiers  
 1..155  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZP762B035"  
 /tissue\_type="melanoma (MeMo cell line)"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_id="762 (synonym: hme12)"  
 /note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

ORIGIN  
 Query Match 100.0%; Score 20; DB 1; Length 155;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
 |||||  
 59 ATGATGGCGCGGAGTGTGA 40

RESULT 4  
 BQ319320 160 bp mRNA linear EST 17-MAY-2002  
 LOCUS QVO-CT0583-101100-491-804 CT0583 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BQ319320  
 ACCESSION BQ319320.1 GI:20925236  
 VERSION BQ319320.1 GI:20925236  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE  
20202663  
PUBMED  
10737800

COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&t2=QV0-CT0583-  
101100-491-a04&t3=2000-11-10&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 55  
High quality sequence stop: 95.  
Location/Qualifiers

## FEATURES

source  
1..160  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1lb="CT0583"  
/note="Organ: colon; Vector: puc18; Site\_1: Sma1; Site\_2:  
Sma1; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 160;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
Db 129 ATGATGCGCGCGAGTGTGA 148

RESULT 5  
BE719607 163 bp mRNA linear EST 12-SEP-2000  
LOCUS RC2-HT0861-310700-011-f06 HT0861 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BE719607  
ACCESSION BE719607  
VERSION BE719607.1 GI:10107872  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 163)  
Diae Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coستا,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente, 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922

Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC2-HT0861-310  
700-011-f06&t3=2000-07-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 163.  
Location/Qualifiers

## FEATURES

source  
1..163  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1lb="HT0861"  
/note="Organ: head neck; Vector: puc18; Site\_1: Sma1;  
Site\_2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 163;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
Db 114 ATGATGCGCGCGAGTGTGA 95

RESULT 6  
CN335092 164 bp mRNA linear EST 16-MAY-2004  
LOCUS 17000532684809 GRN\_ES Homo sapiens cDNA 5', mRNA sequence.  
DEFINITION CN335092  
ACCESSION CN335092  
VERSION CN335092.1 GI:47335026  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 164)  
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,  
Li,Y., Xu,C., Fang,R., Guejler,K., Rao,M.S., Mandalam,R.,  
Lebkowski,J and Stanton,L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6), 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 164 Std Error: 0.00.  
Location/Qualifiers

## FEATURES

source  
1..164  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, cell lines H1, H7, and  
H9"  
/clone\_1lb="GRN ES"  
/note="Toigo et al. primed, full-length enriched cDNA library  
from undifferentiated hES cell lines H1 (p32), H7 (p29),  
and H9 (p26) maintained in feeder-free conditions"

## ORIGIN

Query Match 100.0%; Score 20; DB 7; Length 164;

Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
100 ATGATGCGCGCGAGTGTGA 81

RESULT 7  
BE699907/c 178 bp mRNA linear EST 12-SEP-2000

LOCUS MR0-NN0087-230500-009-d06 NN0087 Homo sapiens cDNA, mRNA sequence.

DEFINITION BE699907  
BE699907.1 GI:10087649

VERSION EST.  
KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 178)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,  
Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=MR0-NN0087-230  
500-009-d06&f3=2000-05-23&f4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 178.  
Location/Qualifiers

1..178  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_1b="NN0087"

/note="Organ: nervous normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

# ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 178;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
111 ATGATGCGCGCGAGTGTGA 92

RESULT 8  
AM575670/c 184 bp mRNA linear EST 15-MAR-2000

DEFINITION UI-HF-BM0-ack-h-02-0-UI.s1 NIH\_MGC\_38 Homo sapiens cDNA clone  
IMAGE:3062234 3', mRNA sequence.  
AM575670  
AM575670.1 GI:7247209

ACCESSION EST.  
Homo sapiens (human)

VERSION Homo sapiens  
SOURCE Homo sapiens

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
1 (bases 1 to 184)

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

TITLE Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Oligo-dt track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. Tissue Procurement: Louis M.  
Staudt, M.D., Ph.D.

COMMENT CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/INLNL at:  
www-bio.llnl.gov/bdpr/image/image.html  
Seq primer: M13 Forward  
POLYA=No

FEATURES Location/Qualifiers

1..184  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3062234"

/tissue\_type="lymph"

/cell\_type="germinal center B cells"

/lab\_host="DH10B (LTI)"

/clone\_1b="NIH MGC 38"

/note="Vector: p773-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(2.5-3.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

# ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
77 ATGATGCGCGCGAGTGTGA 58

RESULT 9  
AU077224/c 185 bp mRNA linear EST 04-MAY-2000

LOCUS AU077224 Sugano cDNA library Homo sapiens cDNA clone Zv61966  
DEFINITION similar to 5'-end region of Chinese hamster nucleolin (C23) mRNA,  
mRNA sequence.

ACCESSION AU077224  
AU077224.1 GI:7439847

VERSION EST.  
Homo sapiens (human)

KEYWORDS Homo sapiens

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 185)  
Suzuki, Y., Ishihara, D., Sasaki, M., Nakagawa, H., Hata, H.,  
Tsunoda, T., Watanabe, M., Komatsu, T., Ota, T., Isogai, T., Suyama, A.  
and Sugano, S.

TITLE Statistical analysis of the 5' untranslated region of human mRNA  
using Oligo-capped cDNA libraries  
JOURNAL Genomics 64 (3), 286-297 (2000)

MEDLINE  
20221373  
PUBMED  
10756096  
COMMENT  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki Y., Yoshimoto-Nakagawa K., Maruyama K., Suyama A. and  
Sugano S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997)  
This clone was obtained from a '5'-end-enriched' cDNA library  
constructed by 'Oligo-Capping' method. The coding region starts  
from the 50 bp upstream to the 3'-end.  
Location/Qualifiers  
1.185  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="Sugano cDNA library"

ORIGIN  
Query Match 100.0%; Score 20; DB 1; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  
1 ATGATGCGCGCGAGTGTCGA 20  
|||||  
137 ATGATGCGCGCGAGTGTCGA 118

RESULT 10  
AW050536/c 205 bp mRNA linear EST 09-MAR-2000  
LOCUS  
wz14a01.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2557992 3'  
DEFINITION  
similar to gb:U60858\_rnal NCICLROLIN (HUMAN); mRNA sequence.  
ACCESSION  
AW050536  
VERSION  
AW050536.1 GI:5912806  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 205)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/HLN at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 2161 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 171.  
Location/Qualifiers  
1.205  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:2557992"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut4"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;

FEATURES  
Source

ORIGIN  
Query Match 100.0%; Score 20; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  
1 ATGATGCGCGCGAGTGTCGA 20  
|||||  
57 ATGATGCGCGCGAGTGTCGA 38

RESULT 11  
W79364 210 bp mRNA linear EST 17-OCT-1996  
LOCUS  
zd72dl1.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone  
DEFINITION  
IMAGE:346197 5' similar to gb:U60858\_rnal NCICLROLIN (HUMAN); mRNA  
sequence.  
ACCESSION  
W79364  
VERSION  
W79364.1 GI:1390153  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 210)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 272 Std Error: 0.00  
Seq primer: mob.REGA+ET  
Location/Qualifiers  
1.210  
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/db\_xref="GDB:1271572"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:346197"  
/sex="unknown"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal heart NBH19W"  
/note="Organ: heart; Vector: pRT3D (pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATCGAAGTGGAGCGCGCCATCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pRT3 vector  
(pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by  
M. Fatima Bonaldo. This library was constructed from the  
same fetus as the fetal lung library, Soares fetal lung  
NBH19W."

ORIGIN  
Query Match 100.0%; Score 20; DB 7; Length 210;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGATGCGCGCGAGTGTGA 20  
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 Db 180 ATGATGCGCGCGAGTGTGA 199

RESULT 12  
 AA263089 215 bp mRNA linear EST 02-JUL-1998  
 LOCUS AA263089/c  
 DEFINITION PMV0457 KGI-a lambda Zap Express cDNA library Homo sapiens CDNA 5',  
 mRNA sequence.  
 ACCESSION AA263089  
 VERSION AA263089.1 GI:1898887  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 TITLE 1 (bases 1 to 215)  
 CLAUDE J. O., LIEW, C. C., DEMPSEY, A. A., CUKERMAN, E., STEWART, A. K.,  
 Na, E., ATKINS, H. I., ISCOVE, N. N. and HAWLEY, R. G.  
 Identification of sequence-tagged transcripts differentially  
 expressed within the human hematopoietic hierarchy  
 Genomics 50 (1), 44-52 (1998)  
 JOURNAL 98292493  
 MEDLINE 9628821  
 COMMENT Contact: Hawley RG  
 Oncology Research Laboratories  
 The Toronto Hospital  
 CRC-424, 67 College St., Toronto, Ontario M5G 2M1, Canada  
 Tel: 416 3403834  
 Fax: 416 3403453  
 Email: r.hawley@utoronto.ca  
 Similar to M60858 nucleolin gene. Clone was randomly picked from  
 KGIa primary library.  
 Seq primer: 5' GAATTTACCTTCCTACTAAAGG 3'  
 High quality sequence stop: 215.  
 Location/Qualifiers  
 1..215  
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 /cell\_type="promyeloblast"  
 /cell\_line="KGI-a"  
 /clone\_lib="KGI-a lambda Zap Express cDNA library"  
 /note="Vector: lambda Zap Express (Stratagene); Site\_1:  
 EcoRI; Site\_2: XhoI; Unidirectional cloning sites:  
 EcoRI-XhoI. mRNA was purified from KGI-a cell line. cDNA  
 was synthesized using an XhoI-0150dT linker primer. EcoRI  
 adaptors were ligated, followed by digestion with XhoI for  
 directional cloning into predigested lambda Zap Express"

ORIGIN  
 Query Match 100.0%; Score 20; DB 1; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGATGCGCGCGAGTGTGA 20  
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 Db 85 ATGATGCGCGCGAGTGTGA 66

RESULT 13  
 BX644913/c 219 bp mRNA linear EST 04-SEP-2003  
 LOCUS BX644913  
 DEFINITION DKFZp78111236.t1 781 (synonym: hlc4) Homo sapiens cDNA clone  
 DKFZp78111236 5', mRNA sequence.  
 ACCESSION BX644913  
 VERSION BX644913.1 GI:34479246  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 TITLE 1 (bases 1 to 219)  
 WAMBUTT, R., HEUBNER, D., MEWES, H. W., WEIL, B., AMID, C., OSANGER, A.,  
 FODD, G., HAN, W. and WIEMANN, S.  
 EST (Wambutt, R., Heubner, D., Mewes, H. W., Weil, B., Amid, C., et al.)  
 Unpublished (2003)  
 JOURNAL  
 COMMENT Contact: MIPS

FEATURES  
 source  
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 /organism="Homo sapiens"  
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 /clone="DKFZp78111236"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="781 (synonym: hlc4)"  
 /note="Vector: pSPort1\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB;  
 cDNA-collection"

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 Best Local Similarity 100.0%; Pred. No. 0.34;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGATGCGCGCGAGTGTGA 20  
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 Db 119 ATGATGCGCGCGAGTGTGA 100

RESULT 14  
 BF757253 220 bp mRNA linear EST 12-JAN-2001  
 LOCUS BF757253  
 DEFINITION U070-CT0583-031100-476-e03 CT0583 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF757253  
 VERSION BF757253.1 GI:12105153  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 TITLE 1 (bases 1 to 220)  
 DIAS NETO, E., GARCIA CORREA, R., VERJOVSKI-ALMEIDA, S., BRIONES, M. R.,  
 NEGAL, M. A., DA SILVA, W. Jr., ZAGO, M. A., BORDIN, S., COSTA, F. F.,  
 GOLDMAN, G. H., CARVALHO, A. F., MATSUKUMA, A., BALTA, G. S., SIMPSON, D. H.,  
 BRUNSTEIN, A., DE OLIVEIRA, P. S., BUCHER, P., JORGENSEN, C. V.,  
 O'HARE, M. J., SOARES, F., BRENTANI, R. R., REIS, L. F., DE SOUZA, S. J. and  
 SIMPSON, A. J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL 20202663  
 MEDLINE 10737800  
 PUBMED  
 COMMENT Contact: Simpson A. J. G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL



(http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV0&e2=QV0-CT0583-031100-476-e03&e3=2000-11-03&e4=1)

Seq primer: puc 18 forward  
High quality sequence start: 21  
High quality sequence stop: 220.  
Location/Qualifiers

## FEATURES

source

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/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_1ib="CT0583"  
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGGTGA 20  
|||||

Db 189 ATGATGGCGCGGAGGTGA 208  
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RESULT 15  
A1185752/c 221 bp mRNA linear EST 29-OCT-1998  
LOCUS qe44e01.x1 Soares fetal\_lung\_NbHL19w Homo sapiens cDNA clone  
DEFINITION IMAGE:1741848 3' similar to gb:M60858\_rna1 NUCLEOLIN (HUMAN); mRNA  
sequence.

ACCESSION A1185752

VERSION A1185752

KEYWORDS A1185752.1 GI:3736390

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Homo sapiens

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 221)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome/Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-r@mail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 954 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 182.

Location/Qualifiers

1..221

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/clone="IMAGE:1741848"

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/lab\_host="DH10B (ampicillin resistant)"

/clone\_1ib="Soares\_fetal\_lung\_NbHL19w"

/note="Organ: lung; Vector: pT773D (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer

(5'-TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT-3'),

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT773 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

## ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 221;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGCGGAGGTGA 20  
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Db 37 ATGATGGCGCGGAGGTGA 18  
|||||

Soares and M. Patricia Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19w."

Search completed: April 12, 2005, 01:18:23  
Job time : 3107 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 11, 2005, 21:24:33 ; Search time 1674 Seconds  
(without alignments)  
578.915 Million cell updates/sec

Title: US-10-797-822-1

Perfect score: 20

Sequence: 1 atgatgagcgagcgagtgatga 20

Scoring table: **MEMO NUC**  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmb1:\*  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pac:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_ey:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	240	6	CQ503225
2	20	100.0	396	6	CQ472921
3	20	100.0	438	6	CQ512072
4	20	100.0	442	6	AR421707
5	20	100.0	442	6	AX982401
6	20	100.0	442	6	BD117260
7	20	100.0	444	6	CQ482090
8	20	100.0	467	6	AX885265
9	20	100.0	467	6	BD024875
10	20	100.0	620	9	HS433862
11	20	100.0	643	9	HS433943
12	20	100.0	716	9	HS433959
13	20	100.0	788	9	HS434235
14	20	100.0	863	9	HS434235
15	20	100.0	1860	6	CQ497033
16	20	100.0	1952	9	BC002343
17	20	100.0	1957	9	BC006494
18	20	100.0	1957	9	BC006516
19	20	100.0	2084	6	CQ725884

C 20	20	100.0	2400	6	CQ850470	CQ850470 Sequence
C 21	20	100.0	2400	9	AK127608	AK127608 Homo sapi
C 22	20	100.0	2532	9	AK000221	AK000221 Homo sapi
C 23	20	100.0	2560	9	AK095897	AK095897 Homo sapi
C 24	20	100.0	2637	6	AX747156	AX747156 Sequence
C 25	20	100.0	2637	9	AK091742	AK091742 Homo sapi
C 26	20	100.0	2655	9	AK122805	AK122805 Homo sapi
C 27	20	100.0	3201	6	CQ490280	CQ490280 Sequence
C 28	20	100.0	3201	6	CQ491168	CQ491168 Sequence
C 29	20	100.0	6112	6	AX347419	AX347419 Sequence
C 30	20	100.0	6112	6	AX349140	AX349140 Sequence
C 31	20	100.0	6112	6	AX657789	AX657789 Sequence
C 32	20	100.0	6112	6	AX659063	AX659063 Sequence
C 33	20	100.0	10942	9	HMMNUCLEO	M60858 Human nucle
C 34	20	100.0	16880	9	AC017104	AC017104 Homo sapi
C 35	18	90.0	134014	8	AC137698	AC137698 Genomic s
C 36	18	90.0	187589	8	AC083942	AC083942 Genomic s
C 37	17	85.0	109148	2	AC138439	AC138439 Takifugu
C 38	17	85.0	110000	2	AC021644_0	AC021644 Homo sapi
C 39	17	85.0	129040	8	AP005466	AP005466 Oryza sat
C 40	17	85.0	157822	8	AP004731	AP004731 Oryza sat
C 41	16	80.0	11349	2	AC012868	AC012868 Drosophila
C 42	16	80.0	11629	1	AE010310	AE010310 Methanopy
C 43	16	80.0	19653	1	AF299336	AF299336 Stigmatel
C 44	16	80.0	84055	3	AC004439	AC004439 Drosophila
C 45	16	80.0	138715	8	OSJN00190	AL662989 Oryza sat

#### ALIGNMENTS

RESULT 1	CQ503225/c	CQ503225	Sequence 35092 from Patent WO0160860.	240 bp	DNA	linear	PAT 30-JAN-2004
LOCUS	CQ503225	CQ503225					
DEFINITION	CQ503225	CQ503225					
ACCESSION	CQ503225	CQ503225					
VERSION	CQ503225.1	GI:41468861					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							
QY							
Db							
RESULT 2							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1  
Schlegel R., Endege, W.O. and Monahan, J.E.  
Genes differentially expressed in human prostate cancer and their  
use  
Patent: WO 0160860-A 4788 23-AUG-2001;  
Millennium Predictive Medicine, Inc. (US)  
Location/Qualifiers  
1. 396  
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Matches 20; Conservative 0; Mismatches 0;

QY 1 ATGATGGCGCGGAGTGTGA 20  
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RESULT 3  
COSI2072/c 438 bp DNA linear PAT 30-JAN-2004  
LOCUS Sequence 43939 from Patent WO0160860.  
DEFINITION COSI2072  
ACCESSION COSI2072.1 GI:41478336  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1  
Schlegel, R., Endege, W.O. and Monahan, J.E.  
Genes differentially expressed in human prostate cancer and their  
use  
Patent: WO 0160860-A 43939 23-AUG-2001;  
Millennium Predictive Medicine, Inc. (US)  
Location/Qualifiers  
1. 438  
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QY 1 ATGATGGCGCGGAGTGTGA 20  
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80 ATGATGGCGCGGAGTGTGA 61

RESULT 4  
AR421707/c 442 bp DNA linear PAT 18-DEC-2003  
LOCUS Sequence 13204 from patent US 6639063.  
DEFINITION AR421707  
ACCESSION AR421707  
VERSION AR421707.1 GI:40176817  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unknown.  
Unclassified.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1 (bases 1 to 442)  
Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.  
EST's and encoded human proteins  
Patent: US 6639063-A 13204 28-OCT-2003;  
Location/Qualifiers  
1. 442

ORIGIN  
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QY 1 ATGATGGCGCGGAGTGTGA 20  
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166 ATGATGGCGCGGAGTGTGA 147

RESULT 5  
AX982401/c 442 bp DNA linear PAT 15-JAN-2004  
LOCUS Sequence 13204 from Patent EP1104808.  
DEFINITION AX982401  
ACCESSION AX982401  
VERSION AX982401.1 GI:40988541  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1  
Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.-Y.  
ESTs and encoded human proteins  
Patent: EP 1104808-A 13204 06-JUN-2001;  
Genset (FR)  
Location/Qualifiers  
1. 442  
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166 ATGATGGCGCGGAGTGTGA 147

RESULT 6  
BD117260/c 442 bp DNA linear PAT 18-SEP-2002  
LOCUS EST and encoded human protein.  
DEFINITION BD117260  
ACCESSION BD117260.1 GI:23212164  
VERSION JP 2002010789-A/9337  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 442)  
Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.  
EST and encoded human protein  
Patent: JP 2002010789-A 9337 15-JAN-2002;  
GENSET CORP  
OS Homo sapiens (human)  
PN JP 2002010789-A/9337  
PD 15-JAN-2002  
PF 07-AUG-2000 JP 2002080989  
PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI  
GIORDANO  
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC  
C12N15/00  
CC EST and encoded human protein

FEATURES  
source  
1.442  
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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 442;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
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Db 166 ATGATGCGCGCGAGTGTGA 147

RESULT 7  
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DEFINITION Sequence 13957 from Patent WO0160860.  
ACCESSION CQ482090  
VERSION CQ482090.1 GI:41447709  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.  
TITLE Genes differentially expressed in human prostate cancer and their  
JOURNAL use  
Patent: WO 0160860-A 13957 23-AUG-2001;  
Millennium Predictive Medicine, Inc. (US)  
LOCATION/Qualifiers  
1.444  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||

Db 70 ATGATGCGCGCGAGTGTGA 51

RESULT 8  
LOCUS AX885265/c 467 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 1128 from Patent EP1033401.  
ACCESSION AX885265  
VERSION AX885265.1 GI:40041253  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Dumas Milne Edwards, J.B., Duclet, A. and Giordano, J.Y.  
TITLE Expressed sequence tags and encoded human proteins  
JOURNAL Patent: EP 1033401-A 1128 06-SEP-2000;  
Genet (FR)  
LOCATION/Qualifiers  
1.467  
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/db\_xref="taxon:9606"

FEATURES  
source

CDS 162..>467  
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Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 163 ATGATGCGCGCGAGTGTGA 144

RESULT 9  
LOCUS BD024875/c 467 bp DNA linear PAT 27-AUG-2002  
DEFINITION Sequence tag and encoded human protein.  
ACCESSION BD024875  
VERSION BD024875.1 GI:22566098  
KEYWORDS JP 2001269182-A/1121.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Edwards, J.B.D.M., Duclet, R. and Jordan, J.Y.  
TITLE 1 (bases 1 to 467)  
JOURNAL Sequence tag and encoded human protein  
Patent: JP 2001269182-A 1121 02-OCT-2001;  
GENSET

COMMENT  
OS Homo sapiens (human)  
PN JP 2001269182-A/1121  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JUAN BAPOTIST DUMAS MILNE EDWARDS, EIMERIC DUCLEIR, JEAN YVES  
PI JORDAN  
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC  
C12N5/10  
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC  
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CC  
FH Key Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 467;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
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Db 163 ATGATGCGCGCGAGTGTGA 144

RESULT 10  
LOCUS HSA338862/c 620 bp DNA linear PRI 18-JUL-2002  
DEFINITION Homo sapiens genomic sequence surrounding Ncti site, clone  
ACCESSION HSA338862  
VERSION AJ338862  
KEYWORDS AJ338862.1 GI:15883280

FEATURES  
source

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 620)
AUTHORS     Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvaasha, S.M.,
            Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
            Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
            Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE       Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL     Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE     22131767
PUBMED      12136098
REFERENCE   2 (bases 1 to 620)
AUTHORS     Zabarovsky, E.R.
TITLE       Direct Submission
JOURNAL     Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
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Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ATGATGGCGCGGAGTGTGA 20
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    78 ATGATGGCGCGGAGTGTGA 59

RESULT 11
HSA339439/c      643 bp      DNA      linear      PRI 18-JUL-2002
LOCUS            Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION       NRI-MASC.
ACCESSION        AJ339439
VERSION          AJ339439.1 GI:15883857
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE        1 (bases 1 to 643)
AUTHORS          Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvaasha, S.M.,
            Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
            Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
            Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE            Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL          Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE          22131767
PUBMED           12136098
REFERENCE        2 (bases 1 to 643)
AUTHORS          Zabarovsky, E.R.
TITLE            Direct Submission
JOURNAL          Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
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ORIGIN

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Query Match      100.0%; Score 20; DB 9; Length 643;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ATGATGGCGCGGAGTGTGA 20
    |||||||
    78 ATGATGGCGCGGAGTGTGA 59

RESULT 12
HSA339590/c      716 bp      DNA      linear      PRI 18-JUL-2002
LOCUS            Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION       NLI-Z021C.
ACCESSION        AJ339590
VERSION          AJ339590.1 GI:15884008
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE        1 (bases 1 to 716)
AUTHORS          Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvaasha, S.M.,
            Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
            Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
            Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE            Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL          Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE          22131767
PUBMED           12136098
REFERENCE        2 (bases 1 to 716)
AUTHORS          Zabarovsky, E.R.
TITLE            Direct Submission
JOURNAL          Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
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            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="NLI-Z021C"
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Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 ATGATGGCGCGGAGTGTGA 20
    |||||||
    78 ATGATGGCGCGGAGTGTGA 59

RESULT 13
HSA342352/c      788 bp      DNA      linear      PRI 18-JUL-2002
LOCUS            Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION       NRI-OE8C.
ACCESSION        AJ342352
VERSION          AJ342352.1 GI:15886769
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE        1 (bases 1 to 788)
AUTHORS          Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvaasha, S.M.,
            Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
            Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
            Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
            NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
TITLE            Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL          Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE          22131767
PUBMED           12136098
REFERENCE        2 (bases 1 to 788)
AUTHORS          Zabarovsky, E.R.
TITLE            Direct Submission
JOURNAL          Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES    source
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ORIGIN

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JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)  
MEDLINE 22131767  
PUBMED 12136098  
REFERENCE 2 (bases 1 to 788)  
AUTHORS Zabarovsky, E.R.  
TITLE Direct Submision  
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,  
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,  
Sweden

FEATURES  
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/clone="NR1-0E8C"

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Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
78 ATGATGCGCGCGAGTGTGA 59

Db

RESULT 14  
HSA342353/c 863 bp DNA linear PRI 18-JUL-2002  
LOCUS HSA342353  
DEFINITION Homo sapiens genomic sequence surrounding NctI site, clone  
NR1-0I12C.  
ACCESSION AJ342353  
VERSION AJ342353.1 GI:15886770  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 863)  
AUTHORS Kutsenko, A.S., Glazulin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,  
Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,  
Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,  
Kiselev, L.L., Maesman, W., Wahlstedt, C. and Zabarovsky, E.R.  
TITLE NotI flanking sequences: a tool for gene discovery and verification  
of the human genome  
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)  
MEDLINE 22131767  
PUBMED 12136098  
REFERENCE 2 (bases 1 to 863)  
AUTHORS Zabarovsky, E.R.  
TITLE Direct Submision  
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,  
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,  
Sweden

FEATURES  
source Location/Qualifiers  
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/clone="NR1-0I12C"

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Query Match. 100.0%; Score 20; DB 9; Length 863;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
78 ATGATGCGCGCGAGTGTGA 59

Db

RESULT 15  
CQ497033/c

LOCUS CQ497033 1860 bp DNA linear PAT 30-JAN-2004  
DEFINITION Sequence 28900 from Patent WO0160860.  
ACCESSION CQ497033  
VERSION CQ497033.1 GI:41462669  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.  
TITLE Genes differentially expressed in human prostate cancer and their  
use  
JOURNAL Patent: WO 0160860-A 28900 23-AUG-2001;  
Millennium Predictive Medicine, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match. 100.0%; Score 20; DB 6; Length 1860;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
133 ATGATGCGCGCGAGTGTGA 114

Db

Search completed: April 12, 2005, 00:24:54  
Job time : 1678 secs

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CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
 CC  
 XX Sequence 240 BP, 65 A, 61 C, 66 G, 48 T, 0 U, 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20  
 Db 116 ATGATGGCGCGGAGTGTGA 97

RESULT 2  
 ACH50285/c  
 ID ACH50285 standard; cDNA, 377 BP.

ACH50285;

13-OCT-2003 (first entry)

Human leukocyte cDNA #1879.

Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.

17-APR-2003.

30-JUL-2001; 2001US-00918995.

30-JUL-2001; 2001US-00918995.

(DRMA/) DRMANAC R T.

(STAC/) STACHE-CRAIN B.

(DICK/) DICKSON M C.

(JONE/) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful  
 as hybridization probes, as oligomers for PCR, for chromosome and gene  
 mapping, in the recombinant production of protein, or in generating  
 antisense DNA or RNA.

Claim 1; SEQ ID NO 37497; 44bp; English.

The invention relates to an isolated polynucleotide comprising any one of  
 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 determined by the technique of SBH (sequencing by hybridisation). Also  
 included is a purified polypeptide comprising a sequence corresponding to  
 a reading frame of the novel polynucleotide. The nucleic acid sequences  
 are useful in diagnostic as expressed sequence tags (EST) for  
 identifying expressed genes or for physical mapping of the human genome,  
 in forensics, in assessing biodiversity, or in identifying mutations  
 responsible for genetic disorders and other traits. The nucleotide  
 sequences are also useful as hybridisation probes, as oligomers for PCR,  
 for chromosome and gene mapping, in the recombinant production of  
 protein, or in generating antisense DNA or RNA. The purified polypeptide

CC is useful for generating antibodies specific for it. The present sequence  
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC [seqdata.uspto.gov/sequence.html?docid=20030073623](http://seqdata.uspto.gov/sequence.html?docid=20030073623)  
 CC  
 XX Sequence 377 BP, 114 A, 102 C, 98 G, 63 T, 0 U, 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGGCGCGGAGTGTGA 20  
 Db 98 ATGATGGCGCGGAGTGTGA 79

RESULT 3  
 ABV04797/c  
 ID ABV04797 standard; cDNA, 396 BP.

ABV04797;

13-SEP-2002 (first entry)

Human prostate expression marker cDNA 4788.

Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 pharmacogenomic marker; gene; ss.

Homo sapiens.

WO200160860-A2.

23-AUG-2001.

20-FEB-2001; 2001WO-US005171.

17-FEB-2000; 2000US-0183319P.

16-MAR-2000; 2000US-0189862P.

25-MAY-2000; 2000US-0207454P.

09-JUN-2000; 2000US-0211314P.

18-JUL-2000; 2000US-0219007P.

13-DEC-2000; 2000US-0255281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of  
 prostate cells and correlating with presence of prostate cancer, useful  
 for detecting presence of prostate cancer, stage of prostate cancer.

Claim 1; Page 824-825; 11750bp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising  
 a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 specification or its complement. (I) is useful for: (a) assessing whether  
 a patient is afflicted with prostate cancer; (b) monitoring the efficacy  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker  
 CC  
 XX Sequence 396 BP, 125 A, 94 C, 103 G, 68 T, 0 U, 6 Other;

Query Match 100.0%; Score 20; DB 5; Length 396;

Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
DB 86 ATGATGCGCGCGAGTGTGA 67

RESULT 4  
ABV43920/c  
ID ABV43920 standard; cDNA; 438 BP.

XX  
AC ABV43920;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 43911.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183119P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of  
XX prostate cells and correlating with presence of prostate cancer, useful  
XX for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 8734; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising  
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
XX specification or its complement. (I) is useful for: (a) assessing whether  
XX a patient is afflicted with prostate cancer; (b) monitoring the  
XX progression of prostate cancer in a patient; (c) assessing the efficacy  
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing  
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;  
XX (e) selecting a composition for inhibiting prostate cancer in a patient;  
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
XX determining whether prostate cancer has metastasized in a patient; (h)  
XX assessing the aggressiveness or indolence of prostate cancer in a patient  
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SEQ Sequence 438 BP; 140 A; 113 C; 118 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 438;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
DB 80 ATGATGCGCGCGAGTGTGA 61

RESULT 5

ABV13966/c  
ID ABV13966 standard; cDNA; 444 BP.

XX  
AC ABV13966;

XX DT 13-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 13957.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183119P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of  
XX prostate cells and correlating with presence of prostate cancer, useful  
XX for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 2327; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising  
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
XX specification or its complement. (I) is useful for: (a) assessing whether  
XX a patient is afflicted with prostate cancer; (b) monitoring the  
XX progression of prostate cancer in a patient; (c) assessing the efficacy  
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing  
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;  
XX (e) selecting a composition for inhibiting prostate cancer in a patient;  
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
XX determining whether prostate cancer has metastasized in a patient; (h)  
XX assessing the aggressiveness or indolence of prostate cancer in a patient  
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SEQ Sequence 444 BP; 151 A; 114 C; 111 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 444;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20  
|||||  
DB 70 ATGATGCGCGCGAGTGTGA 51

RESULT 6  
AAC01130/c  
ID AAC01130 standard; cDNA; 467 BP.

XX  
AC AAC01130;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein 5' EST, SEQ ID NO: 1128.

KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KM gene therapy; chromosome mapping; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-00200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 XX  
 DR P-PSDB; AAG01124.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX  
 XX Claim 1; SEQ ID NO 1128; 71bp + Sequence Listing; English.  
 PS  
 CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. An ORF has been identified within the  
 CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs  
 CC derived from 30 different tissues. EST sequences usually correspond  
 CC mainly to the 3' untranslated region (UTR) of the mRNA because they are  
 CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not  
 CC well suited for isolating cDNA sequences derived from the 5' ends of  
 CC mRNAs and even in those cases where longer cDNA sequences have been  
 CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from  
 CC mRNAs with intact 5' ends and can therefore be used to obtain full length  
 CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,  
 CC gene therapy and chromosome mapping procedures. They are used to obtain  
 CC upstream regulatory sequences and to design expression and secretion  
 CC vectors  
 CC  
 SQ Sequence 467 BP; 133 A; 127 C; 123 G; 84 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;  
 QY 1 ATGATGGCGGCGGAGTGTGA 20  
 |||||  
 DB 163 ATGATGGCGGCGGAGTGTGA 144

RESULT 7  
 ID ACN88171/C  
 ACN88171 standard; DNA; 636 BP.  
 XX  
 AC ACN88171;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Breast cancer related marker, seq id 9321.  
 XX  
 KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003099974-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 PF 18-JUL-2002; 2002US-00198846.  
 XX  
 PR 18-JUL-2001; 2001US-0306220P.

XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Lillie J, Xu Y, Wang Y, Steinmann K;  
 XX  
 DR WPI; 2003-787014/74.  
 XX  
 PT Novel isolated polypeptide associated with breast cancer, useful for  
 PT detecting presence of polypeptide in sample, as a marker for breast  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 9321; 36bp; English.  
 XX  
 CC The invention relates to an isolated polypeptide (I) associated with  
 CC breast cancer which is encoded by a nucleic acid molecule comprising a  
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to  
 CC the polypeptide of the invention. The activity of the polypeptide of the  
 CC invention may be described as cytostatic. The antibody is useful for  
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
 CC invention are useful in the detection of breast tumours. (I) is useful as  
 CC a marker for breast cancer and in breast cancer therapy. Sequences given  
 CC in records ACN/8851-ACN92934 represent nucleic acid markers associated  
 CC with breast cancer. Note: The sequence listing does not form part of the  
 CC specification but may be obtained in electronic format from the USPTO web  
 CC site at [seqdata.uspto.gov/sequence.html?docID=20030999974](http://seqdata.uspto.gov/sequence.html?docID=20030999974)  
 CC  
 SQ Sequence 636 BP; 205 A; 144 C; 180 G; 103 T; 0 U; 4 Other;  
 Query Match 100.0%; Score 20; DB 11; Length 636;  
 Best Local Similarity 100.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0;  
 QY 1 ATGATGGCGGCGGAGTGTGA 20  
 |||||  
 DB 133 ATGATGGCGGCGGAGTGTGA 114

RESULT 8  
 ID ABQ41262  
 ABQ41262 standard; DNA; 1276 BP.  
 XX  
 AC ABQ41262;  
 XX  
 DT 12-JUL-2002 (first entry)  
 XX  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27853.  
 XX  
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
 KW drug; side effect; cancer; central nervous system; cardiovascular;  
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
 KW SNP; cell differentiation; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200218632-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 PF 01-SEP-2001; 2001WO-EP010074.  
 XX  
 PR 01-SEP-2000; 2000DE-01043826.  
 XX  
 PR 05-SEP-2000; 2000DE-01044543.  
 XX  
 PA (EPIC-) EPIDENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K, Guertig D;  
 XX  
 DR WPI; 2002-371829/40.  
 XX  
 PT Determining the degree of cytosine methylation in genomic DNA, useful for  
 PT diagnosis and prognosis, comprises selective hybridization of amplicons  
 PT from chemically treated DNA.

PS Claim 12; 56bp + Sequence Listing; 56bp; German.  
XX  
XX This invention describes a novel method for determining the degree of  
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridized to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridization to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridized to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABO13410-  
CC ABO54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
SQ Sequence 1276 BP; 205 A; 151 C; 442 G; 478 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 1276;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGATGGCGCGGAGTGTGA 20  
DB 582 ATGATGGCGCGGAGTGTGA 601  
|||||  
RESULT 9  
ABO41263/C  
ID ABO41263 standard; DNA; 1276 BP.  
XX  
AC ABO41263;  
XX  
DT 12-JUN-2002 (first entry)  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27854.  
XX  
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;  
KW drug; side effect; cancer; central nervous system; cardiovascular;  
KW gastrointestinal; respiratory system; single nucleotide polymorphism;  
KW SNP; cell differentiation; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200218632-A2.  
XX  
PD 07-MAR-2002.  
XX  
PE 01-SEP-2001; 2001WO-EP010074.  
XX  
PR 01-SEP-2000; 2000DE-01043826.  
PR 05-SEP-2000; 2000DE-01044543.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K, Guetig D;  
XX  
DR WPI; 2002-371829/40.  
XX  
PT Determining the degree of cytosine methylation in genomic DNA, useful for  
PT diagnosis and prognosis, comprises selective hybridization of amplicons  
PT from chemically treated DNA.  
XX  
PS Claim 12; 56bp + Sequence Listing; 56bp; German.  
XX  
CC This invention describes a novel method for determining the degree of

CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a  
CC genomic sample of DNA. The sample is treated chemically to convert  
CC cytosine (C) but not methylated C, to uracil, then part of the genomic  
CC DNA that contains the target C is amplified to form a labeled amplicon.  
CC The amplicon is hybridized to two classes, each with at least one member,  
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the  
CC degree of hybridization to both classes is determined from the label on  
CC the amplicon. From the ratio of labels hybridized to the two classes of  
CC oligomers, the degree of methylation is calculated. The method is used:  
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs  
CC and of a wide range of diseases, e.g. cancer, disorders of the central  
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,  
CC particularly by detecting mutations or single nucleotide polymorphisms  
CC (SNP's); and (ii) for differentiation of cell or tissue types and for  
CC investigating cell differentiation. The method allows the methylation  
CC status of many C residues to be determined simultaneously. ABO13410-  
CC ABO54121 represent genomic DNA sequences used to illustrate the method  
CC for determining the degree of cytosine methylation described in the  
CC disclosure of the invention  
XX  
SQ Sequence 1276 BP; 478 A; 442 C; 151 G; 205 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 1276;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGATGGCGCGGAGTGTGA 20  
DB 695 ATGATGGCGCGGAGTGTGA 676  
|||||  
RESULT 10  
ADP46512/C  
ID ADP46512 standard; DNA; 1716 BP.  
XX  
AC ADP46512;  
XX  
DT 09-SEP-2004 (first entry)  
DE Human colon specific nucleic acid SEQ ID NO:88.  
XX  
KW ds; gene; human; colon specific protein; CSP; CSNA; cytostatic; vaccine;  
KW gene therapy; colon specific nucleic acid; cancer; colon;  
KW chromosome 2q37.1.  
XX  
OS Homo sapiens.  
XX  
FN WO2004050860-A2.  
XX  
PD 17-JUN-2004.  
XX  
PF 04-DEC-2003; 2003WO-US040063.  
XX  
PR 04-DEC-2002; 2002US-0431132P.  
PR 04-DEC-2002; 2002US-0431144P.  
XX  
PA (DIAD-) DIADEXUS INC.  
XX  
PI Macina RA, Turner LR, Sun Y;  
XX  
DR WPI; 2004-480623/45.  
XX  
PT Novel colon specific protein derived from normal and neoplastic colon  
PT cell, useful as vaccine in treating colon cancer and in identifying,  
PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous  
PT disease state in colon.  
XX  
PS Claim 1; SEQ ID NO 88; 547bp; English.  
XX  
XX The invention relates to a novel colon specific protein (CSP) (i) and the  
CC nucleic acid (CSNA) encoding it. A CSP of the invention has cytostatic  
CC activity. The protein is useful as a vaccine, and the nucleic acid may  
CC have a use in gene therapy. A CSP is useful for determining the presence

CC of a colon specific protein in a sample. A CSNA is useful for determining  
 CC the presence of a colon specific nucleic acid (CSNA) in a sample. The CSP  
 CC and CSNA are useful for diagnosing or monitoring the presence and  
 CC metastases of colon cancer in a patient. A method of the invention is  
 CC useful for treating a patient with colon cancer. A CSP and CSNA are  
 CC useful in identifying, diagnosing, monitoring, staging, imaging colon  
 CC cancer and non-cancerous disease state in colon, and as a vaccine for  
 CC treating colon cancer and non-cancerous disease states in colon. The  
 CC present sequence represents a CSNA of the invention.

XX Sequence 1716 BP; 592 A; 324 C; 486 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 1716;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGTGTGA 20  
 DB 152 ATGATGGCGGCGAGTGTGA 133

# RESULT 11

ABV28882/c  
 ID ABV28882 standard; cDNA, 1860 BP.

XX ABV28882;

XX 16-SEP-2002 (first entry)

XX Human prostate expression marker CDNA 28873.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US005171.

XX 17-FEB-2000; 2000US-0183319P.

XX 16-MAR-2000; 2000US-0189863P.

XX 25-MAY-2000; 2000US-0207454P.

XX 09-JUN-2000; 2000US-0211314P.

XX 18-JUL-2000; 2000US-0219007P.

XX 13-DEC-2000; 2000US-0255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JB;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer.

XX Claim 1; Page 6089; 11750P; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 1860 BP; 572 A; 359 C; 462 G; 467 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 1860;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGTGTGA 20  
 DB 133 ATGATGGCGGCGAGTGTGA 114

# RESULT 12

ADP46511/c  
 ID ADP46511 standard; DNA; 2345 BP.

XX ADP46511;

XX 09-SEP-2004 (first entry)

XX Human colon specific nucleic acid SEQ ID NO:87.

XX ds; gene; human; colon specific protein; CSP; CSNA; cytostatic; vaccine;  
 KW gene therapy; colon specific nucleic acid; cancer; colon;

XX Chromosome 2q37.1.

XX Homo sapiens.

XX WO2004050860-A2.

XX 17-JUN-2004.

XX 04-DEC-2003; 2003WO-US040063.

XX 04-DEC-2002; 2002US-0431132P.

XX 04-DEC-2002; 2002US-0431144P.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Turner LR, Sun Y;

XX WPI; 2004-480623/45.

XX Novel colon specific protein derived from normal and neoplastic colon  
 PT cell, useful as vaccine in treating colon cancer and in identifying,  
 PT diagnosing, monitoring, staging, imaging colon cancer and non-cancerous  
 PT disease state in colon.

XX Claim 1; SEQ ID NO 87; 547P; English.

XX The invention relates to a novel colon specific protein (CSP) (I) and the  
 CC nucleic acid (CSNA) encoding it. A CSP of the invention has cytostatic  
 CC activity. The protein is useful as a vaccine, and the nucleic acid may  
 CC have a use in gene therapy. A CSP is useful for determining the presence  
 CC of a colon specific protein in a sample. A CSNA is useful for determining  
 CC the presence of a colon specific nucleic acid (CSNA) in a sample. The CSP  
 CC and CSNA are useful for diagnosing or monitoring the presence and  
 CC metastases of colon cancer in a patient. A method of the invention is  
 CC useful for treating a patient with colon cancer. A CSP and CSNA are  
 CC useful in identifying, diagnosing, monitoring, staging, imaging colon  
 CC cancer and non-cancerous disease state in colon, and as a vaccine for  
 CC treating colon cancer and non-cancerous disease states in colon. The  
 CC present sequence represents a CSNA of the invention.

XX Sequence 2345 BP; 776 A; 418 C; 625 G; 526 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 2345;  
 Best Local Similarity 100.0%; Pred. No. 0.18;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCGGCGAGTGTGA 20  
 DB 152 ATGATGGCGGCGAGTGTGA 133

## RESULT 13

ADRO7433/C

ID ADRO7433 standard; cDNA; 2400 BP.

AC ADRO7433;

DT 04-NOV-2004 (first entry)

Full length human cDNA useful for treating neurological disease Seq 939.

gene; ss: human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; gene or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic; tranquilizer.

OS Homo sapiens.

PN EP1447413-A2.

PD 18-AUG-2004.

PF 12-FEB-2004; 2004EP-00001145.

PR 14-FEB-2003; 2003JP-00102207.

PA 09-MAY-2003; 2003JP-00131452.

(REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Yamamoto J, Nishikawa T, Isomo Y, Sugiyama T, Otsuki T; Wakamatsu A, Ishii S, Nagai K, Irie R;

DR WPI; 2004-583265/57.

P-PSDB; ADR09389.

PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

PS Claim 1; SEQ ID NO 939; 2686bp; English.

CC This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capping method, where none of these CC clones are identical to any known human mRNA. The present invention CC describes an immunosay to identify agonists and antagonists, as well as CC antibodies, antisense molecules and siRNAs that can all be used to bind CC to and modulate expression of the cDNA molecule. As such, these CC molecules are useful for diagnostic markers or therapeutic targets for CC the various diseases or morbid states. In particular, they are useful in CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's CC disease, Parkinson's disease, dementia, short memory and various cancers, CC as well as for maintaining equilibrium of sense or motor function, and CC for treating emotional reaction, fear response and panic. Accordingly, CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, CC cyostatic and tranquilizer activities. This polynucleotide is a full CC length human cDNA sequence of the invention. NOTE: This sequence is not CC given in the sequence listing of the specification but can be obtained on CC CD-ROM from the European Patent Office, Vienna Sub-office.

XX Sequence 2400 BP; 748 A; 413 C; 665 G; 574 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 2400;

Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20

DB 150 ATGATGCGCGCGAGTGTGA 131

## RESULT 14

AAV71745/C

ID AAV71745 standard; cDNA; 2518 BP.

AC AAV71745;

DT 15-MAR-1999 (first entry)

Human V3 loop HIV receptor P95/nucleolin cDNA.

XX HIV receptor; V3 loop; human immunodeficiency virus; retrovirus; XX P95 protein; nucleolin; infection; therapy; diagnosis; ss.

OS Homo sapiens.

OS Key Location/Qualifiers

PN WO9840480-A1.

PD 17-SEP-1998.

PF 12-MAR-1998; 98WO-EP001409.

PR 12-MAR-1997; 97US-0040969P.

PA (INSP) INST PASTEUR.

PA (CNRS) CENT NAT RECH SCI.

PI Hovanesian A, Callebaut C, Krust B, Jacotot E, Muller S;

PI Briand U, Guichard G;

DR WPI; 1999-034588/03.

P-PSDB; AAW84052.

PT New isolated V3 loop HIV receptor - comprises P95/nucleolin, P40/PHAPI and P30/PHAPI proteins, used to develop products for the treatment and prevention of HIV infection.

PS Claim 17; Fig 49(14); 267bp; English.

CC This cDNA sequence codes for the P95 (or nucleolin) protein of the newly CC identified V3 loop HIV receptor. This novel protein complex receptor for CC HIV retroviruses consists of an association of 3 proteins named CC P95/nucleolin, P40/PHAPI and P30/PHAPI (see AAW84052-54). These proteins CC were isolated from human CD4+ CEM T-cell extracts using an affinity CC matrix containing either the pseudopeptide 5(KpsICH2)NPR)-template CC assembled synthetic peptide or a synthetic V3 loop peptide (see CC AAW84055). P95 was identified as nucleolin by amino acid sequence CC analysis. The invention also concerns peptidic or non-peptidic molecules CC having the ability to alter and/or prevent the binding of the novel HIV CC receptor to the HIV retrovirus, and to pharmaceutical and diagnostic CC compositions containing such molecules. Methods are provided for CC screening for new active molecules, and to methods of screening genetic CC defects in the expression of the V3 loop HIV receptor in individuals that CC survive long-term HIV infection or who are HIV-resistant. Such CC genetically defective polynucleotides can be used in gene therapy

XX Sequence 2518 BP; 823 A; 459 C; 711 G; 525 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 2518;

Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGCGCGCGAGTGTGA 20

DB 113 ATGATGCGCGCGAGTGTGA 94

## RESULT 15

AAC92553/C

ID AAC92553 standard; DNA; 2518 BP.

```

XX AAC92553;
XX 27-MAR-2001 (first entry)
XX Human nucleolin DNA.
XX Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
XX ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
XX cell growth; transcriptional repression; replication;
XX signal transduction; chromatin decondensation; Ag-NOR family;
XX nucleolin antibody; systemic connective tissue disease; SLR;
XX systemic lupus erythematosus;
XX scleroderma-like chronic graft versus host disease;
XX expression inhibition; antisense therapy; tumour formation; cancer;
XX inflammation; immune disorder; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 112..2235
XX FT /*tag= a
XX FT /product= "Human nucleolin"
XX US6165786-A.
XX 26-DEC-2000.
XX 03-NOV-1999; 99US-00433699.
XX 03-NOV-1999; 99US-00433699.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Cowsett LM;
XX WPI, 2001-079848/09.
XX P-PSDB; AAB48964.
XX Novel antisense compound targeted to human nucleolin which specifically
XX hybridizes with and inhibits the expression of human nucleolin, useful
XX for modulating the expression of nucleolin in cells.
XX Claim 1; Col 47-52; 41pp; English.
XX This sequence represents DNA encoding human nucleolin. Nucleolin (also
XX known as P92 or C23) is the most abundant nucleolar phosphoprotein in
XX actively growing cells. Nucleolin primarily participates in ribosome
XX biogenesis and transport of ribosomal components, being able to
XX transiently bind to pre-ribosomes in the nucleolus via a
XX ribonucleoprotein consensus sequence. However, it has also been shown to
XX be involved in cytokinesis, nucleogenesis, cell proliferation and growth,
XX transcriptional repression, replication, signal transduction, and
XX chromatin decondensation. Nucleolin is a member of the Ag-NOR (active
XX ribosomal gene located in the nucleolar organizer region) family of
XX proteins which are markers of active ribosomal genes, and whose
XX expression is associated with the prediction of tumour growth rate. The
XX presence of antibodies against nucleolin are associated with systemic
XX connective tissue diseases such as systemic lupus erythematosus (SLE) and
XX scleroderma-like chronic graft versus host disease. The invention relates
XX to antisense oligonucleotides targeted to the nucleolin gene, which
XX inhibit its expression. A series of oligonucleotides (AAC92560-C92639)
XX were designed to target different regions of the human nucleolin mRNA,
XX and were analysed for their effect on nucleolin mRNA levels by
XX quantitative real-time PCR. The oligonucleotides of the invention are
XX useful for diagnosis, prevention and treatment of conditions associated
XX with nucleolin expression, such as tumour formation, immune disorders and
XX inflammation
XX Sequence 2518 BP; 823 A; 459 C; 711 G; 525 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 4; Length 2518;
XX Best Local Similarity 100.0%; Pred. No. 0.18;

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCGCGCGGAGTGTGA 20  
 |||||  
 Db 113 ATGATCGCGCGGAGTGTGA 94

Search completed: April 11, 2005, 23:56:49  
 Job time : 432 secs